

Appendix I

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## Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).  
You can also have a look at a sample screen of LALNVIEW and access its documentation.

### Results of SIM with:

Sequence 1: SeqID4, (226 residues)  
Sequence 2: E.coli, (226 residues)

### using the parameters:

Comparison matrix: BLOSUM62  
Number of alignments computed: 20  
Gap open penalty: 12  
Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

68.5% identity in 216 residues overlap; Score: 745.0; Gap frequency: 0.0%

```
SeqID4,      9  RLCRTLGYEFNNIELLIQALTHRSAANKHNERLEFLGDSILSIAISDALYHQFPKATEGD
E.coli,      8  RLQRKLGYT FNHQELLQOALTHRSASSKHNERLEFLGDSILSYVIANALYHRFPRVDEGD
               ** * *** **  *** *****  *****  *  **** *  ***

SeqID4,     69  LSRMRATLVKGD TLTIIAKEFKIGDYLYLGP GELKSGGFRRESILADAVEAII GAVYLD A
E.coli,     68  MSRM RATLV RGNTLAELAREFELGECLRLGP GELKSGGFRRESILADTVEALIGGVFLDS
               ***** * **  * ** *  *  *****  **** *  *  **

SeqID4,    129  DIEVCRKLLLSWYQERLAEIKPGINQKDPKTI LQEY LQGFKKPLPDYQVVAVEGEAHDQT
E.coli,    128  DIQTVEKLILN WYQTRLDEISPGDKOKDPKTRLQEY LQGRHLPLPTYL VVQVRGEAHDQE
               **  * * * * *  * * *  *  *  *  *  *  *  *  *  *  *  *  *  *

SeqID4,    189  FTVECKISELDKVV TGVASSRRKAEQLAA AQVLELL
E.coli,    188  FTIHCQVSG LSEP VVG TGSSRRKAEQAAAEQAL KKL
               ** * * *  * *  *****  * * *  *
```

35.3% identity in 17 residues overlap; Score: 24.0; Gap frequency: 0.0%

```
SeqID4,    104  SGGFRRESILADAVEAI
E.coli,    204  TGSSRRKAEQAAAEQAL
               *  **  * * *
```

41.7% identity in 12 residues overlap; Score: 22.0; Gap frequency: 0.0%